

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:32:16 ; Search time 1837.47 Seconds
(without alignments)
1378.042 Million cell updates/sec

Title: US-09-719-017A-1
Perfect score: 121
Sequence: 1 gaattccctgtgacaatca.....tatctaagaagaataacttaca 121

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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22: em_ov:*
23: em_pat:*
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26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
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1	121	100.0	121	6	AX008752	Sequence 1 from Patent WO9964607.	121 bp	DNA	linear	PAT 06-SEP-2000
2	121	100.0	1793	6 <td>AX008753</td> <td>Sequence 1 from Patent WO9964607.<td>121 bp</td><td>DNA<th>linear</th><th>PAT 06-SEP-2000</th></td></td>	AX008753	Sequence 1 from Patent WO9964607. <td>121 bp</td> <td>DNA<th>linear</th><th>PAT 06-SEP-2000</th></td>	121 bp	DNA <th>linear</th> <th>PAT 06-SEP-2000</th>	linear	PAT 06-SEP-2000
3	121	100.0	1793	6 <td>AX025996</td> <td>Sequence 1 from Patent WO9964607.<td>121 bp</td><td>DNA<th>linear</th><th>PAT 06-SEP-2000</th></td></td>	AX025996	Sequence 1 from Patent WO9964607. <td>121 bp</td> <td>DNA<th>linear</th><th>PAT 06-SEP-2000</th></td>	121 bp	DNA <th>linear</th> <th>PAT 06-SEP-2000</th>	linear	PAT 06-SEP-2000
4	92.8	76.7	118	6 <td>A06104</td> <td>Insertion f</td> <td></td> <td></td> <td></td> <td></td>	A06104	Insertion f				
5	92.8	76.7	118	6 <td>A09134</td> <td>Nucleotide</td> <td></td> <td></td> <td></td> <td></td>	A09134	Nucleotide				
6	79.4	65.6	215	6 <td>A03764</td> <td>Synthetic</td> <td></td> <td></td> <td></td> <td></td>	A03764	Synthetic				
7	47	38.8	146	6 <td>A29213</td> <td>Synthetic</td> <td></td> <td></td> <td></td> <td></td>	A29213	Synthetic				
8	43.6	36.0	90	6 <td>E00407</td> <td>DNA coding</td> <td></td> <td></td> <td></td> <td></td>	E00407	DNA coding				
9	43.6	36.0	357	6 <td>AR172799</td> <td>DNA coding</td> <td></td> <td></td> <td></td> <td></td>	AR172799	DNA coding				
10	43.6	36.0	357	6 <td>BD000394</td> <td>DNA encod</td> <td></td> <td></td> <td></td> <td></td>	BD000394	DNA encod				
11	43.2	35.7	1519	6 <td>E31303</td> <td>Process for</td> <td></td> <td></td> <td></td> <td></td>	E31303	Process for				
12	43	35.5	262	1	ECOTRPRO	E.coli trp				
13	43	35.5	269	12	SYNDVA	Synthetic p				
14	42.8	35.4	63	6 <td>E00405</td> <td>DNA coding</td> <td></td> <td></td> <td></td> <td></td>	E00405	DNA coding				
15	42.4	35.0	44	6 <td>A12512</td> <td>trp promote</td> <td></td> <td></td> <td></td> <td></td>	A12512	trp promote				
16	42.2	34.9	118	6 <td>A17072</td> <td>oligonucleo</td> <td></td> <td></td> <td></td> <td></td>	A17072	oligonucleo				
17	42.2	34.9	118	6 <td>A17463</td> <td>oligonucleo</td> <td></td> <td></td> <td></td> <td></td>	A17463	oligonucleo				
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19	42.2	34.9	118	6 <td>AR014440</td> <td>Sequence</td> <td></td> <td></td> <td></td> <td></td>	AR014440	Sequence				
20	42.2	34.9	118	6 <td>AR059827</td> <td>Sequence</td> <td></td> <td></td> <td></td> <td></td>	AR059827	Sequence				
21	42.2	34.9	118	6 <td>I11886</td> <td>Sequence 53</td> <td></td> <td></td> <td></td> <td></td>	I11886	Sequence 53				
22	42.2	34.9	305	6 <td>A76225</td> <td>Sequence 17</td> <td></td> <td></td> <td></td> <td></td>	A76225	Sequence 17				
23	42	34.7	47	6 <td>A11701</td> <td>oligonucleo</td> <td></td> <td></td> <td></td> <td></td>	A11701	oligonucleo				
24	42	34.7	47	6 <td>A15884</td> <td>oligonucleo</td> <td></td> <td></td> <td></td> <td></td>	A15884	oligonucleo				
25	42	34.7	74	6 <td>A24959</td> <td>trp operon</td> <td></td> <td></td> <td></td> <td></td>	A24959	trp operon				
26	42	34.7	74	6 <td>A27465</td> <td>oligonucleo</td> <td></td> <td></td> <td></td> <td></td>	A27465	oligonucleo				
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31	42	34.7	84	6 <td>A15698</td> <td>trp promote</td> <td></td> <td></td> <td></td> <td></td>	A15698	trp promote				
32	42	34.7	86	6 <td>A15697</td> <td>trp promote</td> <td></td> <td></td> <td></td> <td></td>	A15697	trp promote				
33	42	34.7	99	6 <td>A15714</td> <td>pMT 501 Hae</td> <td></td> <td></td> <td></td> <td></td>	A15714	pMT 501 Hae				
34	42	34.7	101	6 <td>A15715</td> <td>oligonucleo</td> <td></td> <td></td> <td></td> <td></td>	A15715	oligonucleo				
35	42	34.7	103	6 <td>A15336</td> <td>Synthetic t</td> <td></td> <td></td> <td></td> <td></td>	A15336	Synthetic t				
36	42	34.7	103	6 <td>I06143</td> <td>Sequence 33</td> <td></td> <td></td> <td></td> <td></td>	I06143	Sequence 33				
37	42	34.7	103	6 <td>I07537</td> <td>Sequence 33</td> <td></td> <td></td> <td></td> <td></td>	I07537	Sequence 33				
38	42	34.7	103	6 <td>I08035</td> <td>Sequence 11</td> <td></td> <td></td> <td></td> <td></td>	I08035	Sequence 11				
39	42	34.7	103	6 <td>I08091</td> <td>Sequence 6</td> <td></td> <td></td> <td></td> <td></td>	I08091	Sequence 6				
40	42	34.7	103	6 <td>I08582</td> <td>Sequence 31</td> <td></td> <td></td> <td></td> <td></td>	I08582	Sequence 31				
41	42	34.7	103	6 <td>I09296</td> <td>Sequence 9</td> <td></td> <td></td> <td></td> <td></td>	I09296	Sequence 9				
42	42	34.7	105	6 <td>A15335</td> <td>Synthetic t</td> <td></td> <td></td> <td></td> <td></td>	A15335	Synthetic t				
43	42	34.7	105	6 <td>E01081</td> <td>DNA sequenc</td> <td></td> <td></td> <td></td> <td></td>	E01081	DNA sequenc				
44	42	34.7	105	6 <td>E01711</td> <td>DNA sequenc</td> <td></td> <td></td> <td></td> <td></td>	E01711	DNA sequenc				
45	42	34.7	105	6 <td>E01714</td> <td>DNA sequenc</td> <td></td> <td></td> <td></td> <td></td>	E01714	DNA sequenc				

ALIGNMENTS

RESULT 1
AX008752
LOCUS AX008752 121 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent WO9964607.
ACCESSION AX008752
VERSION AX008752.1 GI:9996243
KEYWORDS
SOURCE
ORGANISM Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.

REFERENCE 1 (bases 1 to 121)
AUTHORS Favre-Bulle,O., Guitton,C. and Pierrard,J.
TITLE Industrial method for producing heterologous proteins in e.coli and strains useful for said method
JOURNAL Patent: WO 9964607-A 1 16-DEC-1999;
FAVRE BULLE OLIVIER (FR); GUITTON CAROLE (FR); PIERRARD JEROME (FR); RHONE POULENC NUTRITION ANIMAL (FR)
FEATURES
source
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/organism="Escherichia coli"
/db_xref="taxon:562"

BASE COUNT 37 a 27 c 23 g 34 t

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Best Local Similarity 100.0%; Pred. No. 6.3e-32;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaattccctgtgacaataatcatcgaactagtagtaactagcgaactgtgctgagg 60
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DB 1 GAATTCCTGTGACAAATTAATCATCGAAGTAACTAGTACCGACCTGGCTGCAGG 60
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QY 61 tcgacctgagccaaactgtggcgcatacatcaatctgttactaaggaaacttac 120
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DB 61 TCGACCTGCAGCCAGCTGGCGCATCATCATCTGTATCTAAGAAATACTTAC 120
|||||
QY 121 a 121
|
DB 121 A 121

RESULT 2

AX008753

LOCUS

DEFINITION Sequence 2 from Patent WO9964607.

ACCESSION AX008753

VERSION AX008753.1 GI:9996244

KEYWORDS

SOURCE

ORGANISM

synthetic construct.
artificial sequence.
1 (bases 1 to 1793)

REFERENCE

AUTHORS

TITLE

JOURNAL

FAVRE BULLE OLIVIER (FR); GUITTON C. and PIERARD J.
Industrial method for producing heterologous proteins in e.coli and
strains useful for said method
Patent: WO 9964607-A 2 16-DEC-1999;
FAVRE BULLE OLIVIER (FR); GUITTON CAROLE (FR); PIERARD JEROME
(FR); RHONE POULENC NUTRITION ANIMAL (FR)

FEATURES

source

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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="cassette d'expression"
123..1193
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC07435.1"
/db_xref="GI:9996245"
/translation="MOTRKIVRAAVQASPNYDLATGVDTIELARQARDEGCDLIY
FGEWLPDGPYHVMGAPAMSLKTSARYANSLSDSAEFORIAOAAATLGFIALGY
SERSGSLYLGGCLIDDKGOMLSRRKLPVHERVYEGEYAROLIVSDRELGRVGA
LCWEHLSPKSLVALYSQHEAIIHAAPSEFSLYSQAHLSAKYMMASQIYSVEGQC
FTIASSVYDETLDMLEVEGHNASLKVGGSSMIFAPDGTTLAPYLPDAEGILIA
DLMEEIAFAKAIINDPVGHYSKPEATRIYLDLGHREPMTRVHYSKSVIOEAPPEPVOS
TAAPVAVSQTODSDTLVQEPS"

CDS

BASE COUNT 412 a 527 c 478 g 376 t
ORIGIN

Query Match 100.0%; Score 121; DB 6; Length 1793;
Best Local Similarity 100.0%; Pred. No. 9.9e-32;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaattccctgtgacaataatcatcgaactagtagtaactagcgaactgtgctgagg 60
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QY 61 tcgacctgagccaaactgtggcgcatacatcaatctgttactaaggaaacttac 120
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DB 61 TCGACCTGCAGCCAGCTGGCGCATCATCATCTGTATCTAAGAAATACTTAC 120
|||||
QY 121 a 121
|
1

Db 121 A 121

RESULT 3

AX025996

LOCUS

DEFINITION Sequence 1 from Patent FR2787121.

ACCESSION AX025996

VERSION AX025996.1 GI:10187454

KEYWORDS

SOURCE

ORGANISM

Alcaligenes faecalis.
Alcaligenes faecalis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;

REFERENCE

AUTHORS

JOURNAL

1 (bases 1 to 1793)
FAVRE B.O., Pierard J. and Batisse D.N.
Patent: FR 2787121-A 1 16-JUN-2000;
AVENTIS CROSCIENCE (FR)

FEATURES

source

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/db_xref="taxon:511"
123..1193
/note="unnamed protein product"
/codon_start=1
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/db_xref="GI:10187455"
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FGEWLPDGPYHVMGAPAMSLKTSARYANSLSDSAEFORIAOAAATLGFIALGY
SERSGSLYLGGCLIDDKGOMLSRRKLPVHERVYEGEYAROLIVSDRELGRVGA
LCWEHLSPKSLVALYSQHEAIIHAAPSEFSLYSQAHLSAKYMMASQIYSVEGQC
FTIASSVYDETLDMLEVEGHNASLKVGGSSMIFAPDGTTLAPYLPDAEGILIA
DLMEEIAFAKAIINDPVGHYSKPEATRIYLDLGHREPMTRVHYSKSVIOEAPPEPVOS
TAAPVAVSQTODSDTLVQEPS"

CDS

BASE COUNT 412 a 527 c 478 g 376 t
ORIGIN

Query Match

100.0%; Score 121; DB 6; Length 1793;
Best Local Similarity 100.0%; Pred. No. 9.9e-32;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaattccctgtgacaataatcatcgaactagtagtaactagcgaactgtgctgagg 60
|||||
DB 1 GAATTCCTGTGACAAATTAATCATCGAAGTAACTAGTACCGACCTGGCTGCAGG 60
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QY 61 tcgacctgagccaaactgtggcgcatacatcaatctgttactaaggaaacttac 120
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DB 61 TCGACCTGCAGCCAGCTGGCGCATCATCATCTGTATCTAAGAAATACTTAC 120
|||||
QY 121 a 121
|
DB 121 A 121

RESULT 4

A06104

LOCUS

DEFINITION Insertion fragment to produce pfc80.

ACCESSION A06104

VERSION A06104.1 GI:345112

KEYWORDS

SOURCE

ORGANISM

synthetic construct.
artificial sequence.
1 (bases 1 to 118)

REFERENCE

AUTHORS

JOURNAL

NEW DERIVATIVES OF HUMAN/BOVINE BASIC FIBROBLAST GROWTH FACTOR
Patent: WO 9002800-A 10 22-MAR-1990;

FEATURES

source

1..118
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BASE COUNT	37	a	25	c	21	g	35	t
ORIGIN	/db_xref="taxon:32630"							

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Best Local Similarity	92.5%;	Pred. No. 5.4e-22;		
Matches 111; Conservative	0;	Mismatches 2;	Indels 7;	Gaps 1

OY 2 aatccctgttgacaatcatcacyactagttaacagtcgcaagttggctgcaggt 6L
 | | |||||
Db 2 ATTCCCTGTGACAAATTATCATCGAAGCTAGTTACTAGTAGCCAGCTTGCGTCAGGT 6L

OY 62 cgacctgcagccaagccttggcatatccaatcaatgtttatctaagsaatacttaca 12L
||| ||||||||||||||||||||||||||||||||||||||||
Db 62 CGA-----CCAAGCTGGGCATACATTCATCAATTGTATATCAAGAATACTTTACA 114

RESULT	5			
A09134				
LOCUS	A09134	118 bp	DNA	linear
DEFINITION	Nucleotide sequence	15 from patent number	EP0363675.	PAT 23-AUG-1993

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 118)	Bergonzoni, L., Isacchi, A., Sarmientos, P. and Caulet, G.	New derivatives of human/bovine basic Fibroblast growth factor	Patent: EP 0363675-A 15 18-APR-1990;
			FARMITALIA CARLO ERBA S.r.l.

FEATURES	SOURCE	location/Qualifiers
		1..118
		/organism="unidentified"
		/db_xref="taxon:32644"
BASE COUNT	37	a 25 c 21 g 3
ORIGIN		

Query Match	76.7%;	Score 92.8;	DB 6;	Length 118;
Best Local Similarity	92.5%;	Pred. No. 5.4e-22;		
Matches 11;	Conservative	0;	Mismatches 2;	Indels 7;
				Gaps 1

[illegible]

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Oy      62  cgagctgcagccaagcttgggcatacatcatcaatgttatactaagaaatacttaca 121
        |||  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      62  CGA-----CCAAGCTTGGGCATACATTCATCAATTTATCTTAAGGAATACTTACA 114

```

RESULT	6			
LOCUS	A03764	215 bp	DNA	linear
DEFINITION	A03764 Synthetic (pXL288) gene for signal peptide PAM-SAH. PAT 27-NOV-1993			

VERSION	A03764.1	GI:490350
KEYWORDS		
SOURCE	synthetic construct.	
ORGANISM	synthetic construct	
REFERENCE	artificial sequence.	
AUTHORS	1 (bases 1 to 215)	
TITLE	Latta, M., Mayaux, J.F. and Sarmientos, P	
JOURNAL	Method for the synthesis of mature human serum albumin	
GENETICA	Patent: EP 0236210-A 11 09-SEP-1987;	

FEATURES	location/Qualifiers
source	1. .215
	/organism="synthetic construct"
	/db_xref="taxon:32630"

BASE COUNT	61 a	48 c	45 g	61 t
ORIGIN				

Query Match	65.6%;	Score 79.4;	DB 6;	Length 215;
Best Local Similarity	98.8%;	Pred. No. 3.2e-17;		
Matches 80;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy 1 gaattccctgttgacaaltaatcatcgacaactagttaactagtacgcagcttggcgcagg 600
|||||
Db 1 GAATTCCTGTGACAALTAATCATCGACAAGTAGTTAAGTAGACGACGCTTGGCTCAGG 600

2Y	61	tcgacctgcagccaagcttg	81
Db	61	TCGACCTGCAGCCAAGCTTCG	81

RESULT	7		
A29213			
LOCUS	A29213	146 bp	DNA linear
DEFINITION	Synthetic DNA (5' region of human FGF receptor gene) from patent WO9111459.		

```

VERSION      A29213.1  GI:1248934
KEYWORDS     .
SOURCE       synthetic construct.
ORGANISM     synthetic construct
REFERENCE    1 (bases 1 to 146)

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TITLE	EXTRACELLULAR FORM OF THE HUMAN FIBROBLAST GROWTH FACTOR RECEPTOR
JOURNAL	Patent: WO 9111459-A 8 08-AUG-1991;
FEATURES	Location/Qualifiers

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source      1. 146
             /organism="synthetic construct"
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BASE COUNT  32 a      44 c      36 g      34 t
ORIGIN

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Query Match	38.8%	Score 47	DB 6	Length 146
Best Local Similarity	100.0%	Pred. No.	7.9e-06	
Matches 47	Conservative 0	Mismatches 0	Indels 0	Gaps 0

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Qy 75 agcctgggcatacatccaatcaatctgttatctaaggaataacttaca 121
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Db 1 AGCTGGGCATACATCAATCAATTGTTATCTAAGGAATACTTACA 47

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RESULT	8		
E00407		90 bp	PAT 29-SEP-1991
LOCUS	E00407	RNA	linear
DEFINITION	DNA coding for tnp promoter/operator of pYN6.		
VERSION	E00402		

VERSION	E00407.1	GI:21686590
KEYWORDS	JP 1985160887-A/3.	
SOURCE	unidentified plasmid.	
ORGANISM	unidentified plasmid	
REFERENCE	1 (bases 1 to 90)	
AUTHORS	Nakagawa, Y., Uno, S., Nagai, M. and Arimura, H.	
TITLE		
JOURNAL	Patent: JP 1985160887-A 3 22-AUG-1985;	
COMMENT	OS plasmid	

PI NAKAGAWA YUKIMITSU, UNO SHUSEI, NAGAI MASANORI, PI ARIMURA
HINOBUKI
PC C12N15.00//C07H21/04;
CC strandedness: Single;
CC topology: Linear;

Query Match	35.7%	Score 43.2	DB 6	Length 1519
Best Local Similarity	93.8%	Pred. NO. 0.00026		
Matches 45	Conservative 0	Mismatches 3	Indels 0	Gaps 0
Qy	4	ttccctgttgacattatcatcatcgactagttactactagtcagcgact	51	
Db	2	ttccctgttgacattatcatcatcgactagttactactagtcagcgact	49	

RESULT 12
ECOTRPPRO 62 bp DNA linear BCT 26-APR-1993
LOCUS E.coli trp promoter region.
DEFINITION K01792
ACCESSION K01792.1 GI:148058
VERSION mutational analysis; promoter region; trp operon.
KEYWORDS E.coli DNA.
SOURCE Escherichia coli
ORGANISM Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
REFERENCE 1 (bases 1 to 62)
AUTHORS Russell,D.R. and Bennett,G.N.
TITLE Construction and analysis of in vivo activity of E. coli promoter
JOURNAL hybrids and promoter mutants that alter the -35 to -10 spacing
MEDLINE Gene 20, 231-243 (1982)
COMMENT 83158761
[1] examines the efficiency of gene expression in E.coli if the
distance between the -35 and -10 regions is increased and also when
the -35 region from one and the -10 region from another gene are
recombined to form a hybrid promoter region. In every case it was
found that the spacing between these two regions was of prime
importance and can not be greater than 18 bp in a functional
promoter.
FEATURES
source Location/Qualifiers
1..62
-35_signal /organism="Escherichia coli"
-10_signal /db_xref="taxon:562"
BASE COUNT 20..25
17 a 43..48
17 a 19 c 10 g 16 t
ORIGIN 27.7 min on K12 map.
Query Match 35.5%; Score 43; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 15 CCCTGTTGACATTAATCATCGAAGTAACTAGTACGACG 57
RESULT 13
SYNDDVA 269 bp DNA linear SYN 27-APR-1993
LOCUS SYNDDVA
DEFINITION Synthetic plasmid pSL1 DNA fragment.
ACCESSION M31473
VERSION M31473.1 GI:208822
KEYWORDS
SOURCE Synthetic DNA, clone pSL1.
ORGANISM unidentified cloning vector.
REFERENCE 1 (bases 1 to 269)
AUTHORS Laflamme,S.E., Kramer,F.R. and Mills,D.R.
TITLE Comparison of pausing during transcription and replication
JOURNAL Nucleic Acids Res. 13, 8425-8440 (1985)
MEDLINE 86093652
FEATURES
source Location/Qualifiers
1..269
/organism="unidentified cloning vector"
/db_xref="taxon:45196"
BASE COUNT 49 a 92 c 83 g 45 t
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Query Match 35.5%; Score 43; DB 12; Length 269;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 6 ccctgttgacaattaatcatcgactagtaactagtagcag 48
|||||

DB 7 CCCTGTTGACATTAATCATCGAAGTAACTAGTACGACG 49
RESULT 14
E00405 63 bp RNA linear PAT 29-SEP-1997
LOCUS E00405
DEFINITION DNA coding for trp promoter.
ACCESSION E00405
VERSION E00405.1 GI:216868
KEYWORDS JP 1985160887-A/1
SOURCE unidentified plasmid.
ORGANISM unidentified plasmid.
REFERENCE 1 (bases 1 to 63)
AUTHORS Nakagawa,Y., Uno,S., Nagai,M. and Aritmura,H.
TITLE VECTOR
JOURNAL Patent: JP 1985160887-A 1 22-AUG-1985;
COMMENT GREEN CROSS CORP:THE
OS plasmid
PN JP 1985160887-A/1
PD 22-AUG-1985
PF 02-FEB-1984 JP 1984018133
PI NAKAGAWA YUKIMITSU, UNO SHUSEI, NAGAI MASANORI, PI ARIMURA
HIROBUMI
PC C12N15/00//C07H21/04;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
FH key Location/Qualifiers
FH
FT -35_signal 5..10
FT -10_signal 28..33
FT RBS 57..60.
FEATURES
source Location/Qualifiers
1..63
/organism="unidentified plasmid"
/db_xref="taxon:45202"
BASE COUNT 22 a 13 c 11 g 17 t
ORIGIN
Query Match 35.4%; Score 42.8; DB 6; Length 63;
Best Local Similarity 95.7%; Pred. No. 0.00021;
Matches 44; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB 6 ccctgttgacaattaatcatcgactagtaactagtagcagct 51
|||||
DB 1 CCCTGTTGACATTAATCATCGAAGTAACTAGTACGACGAGTT 46
RESULT 15
A12512 44 bp DNA linear PAT 05-JAN-1994
LOCUS A12512
DEFINITION trp promoter and transcriptional start site.
ACCESSION A12512
VERSION A12512.1 GI:491382
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 44)
AUTHORS
TITLE TRANSLATION OF mRNA
JOURNAL Patent: WO 8707644-A 19 17-DEC-1987;
MEDLINE
FEATURES
source Location/Qualifiers
1..44
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 15 a 8 c 7 g 14 t
ORIGIN
Query Match 35.0%; Score 42.4; DB 6; Length 44;
|||||

Best Local Similarity 97.7%; Pred. No. 0.00027;
 Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 8 cgttgacaattaatcattgaaactgtaactagtagcgagctt 51
 |||||||||||||||||||||||||||||||||||
 Db 1 CTGTTGACAAATTATATCATCGAACTAGTACTAGTACGAAGCTT 44

Search completed: September 8, 2002, 00:37:47
 Job time: 7531 sec